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OIQE

RAW SEQUENCE LISTING

DATE: 10/19/2000

PATENT APPLICATION: US/09/676,718

TIME: 11:24:31

Input Set : A:\56113.app

Output Set: N:\CRF3\10192000\I676718.raw

3 <110> APPLICANT: Gladyshev, V. et al.
 5 <120> TITLE OF INVENTION: Mammalian selenoprotein differentially expressed in
 6 tumor cells
 8 <130> FILE REFERENCE: 56113
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/676,718
 C--> 11 <141> CURRENT FILING DATE: 2000-09-28
 13 <150> PRIOR APPLICATION NUMBER: 60/080,850
 14 <151> PRIOR FILING DATE: 1998-04-06
 16 <150> PRIOR APPLICATION NUMBER: PCT/US99/07560
 17 <151> PRIOR FILING DATE: 1999-04-06
 19 <160> NUMBER OF SEQ ID NOS: 15
 21 <170> SOFTWARE: PatentIn Ver. 2.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 162
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: SITE
 30 <222> LOCATION: (93)
 31 <223> OTHER INFORMATION: Xaa represents selenocysteine
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 35 1 5 10 15
 37 Leu Leu Leu Ala Thr Val Leu Gln Ala Val Ser Ala Phe Gly Ala Glu
 38 20 25 30
 40 Phe Ser Ser Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser Asn Leu Leu
 41 35 40 45
 43 Cys Ser Ser Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu Gln Leu Asp
 44 50 55 60
 46 Pro Asp Cys Arg Gly Cys Cys Gln Glu Glu Ala Gln Phe Glu Thr Lys
 47 65 70 75 80
 49 Lys Leu Tyr Ala Gly Ala Ile Leu Glu Val Cys Gly Xaa Lys Leu Gly
 50 85 90 95
 52 Arg Phe Pro Gln Val Gln Ala Phe Val Arg Ser Asp Lys Pro Lys Leu
 53 100 105 110
 55 Phe Arg Gly Leu Gln Ile Lys Tyr Val Arg Gly Ser Asp Pro Val Leu
 56 115 120 125
 58 Lys Leu Leu Asp Asp Asn Gly Asn Ile Ala Glu Glu Leu Ser Ile Leu
 59 130 135 140
 61 Lys Trp Asn Thr Asp Ser Val Glu Glu Phe Leu Ser Glu Lys Leu Glu
 62 145 150 155 160
 64 Arg Ile
 68 <210> SEQ ID NO: 2
 69 <211> LENGTH: 1244
 70 <212> TYPE: DNA
 71 <213> ORGANISM: Homo sapiens
 73 <220> FEATURE:

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74 <221> NAME/KEY: CDS
75 <222> LOCATION: (5)..(493)
77 <220> FEATURE:
78 <221> NAME/KEY: misc_feature
79 <222> LOCATION: (281)..(283)
80 <223> OTHER INFORMATION: TGA codon codes for selenocysteine, Xaa
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84 Met Ala Ala Gln Pro Ser Gly Cys Leu Val Pro Ala Phe Gly Leu
85 1 5 10 15
87 cgg ttg ttg ttg gcg act gtg ctt caa gcg gtg tct gct ttt ggg gca 97
88 Arg Leu Leu Leu Ala Thr Val Leu Gln Ala Val Ser Ala Phe Gly Ala
89 20 25 30
91 gag ttt tca tgc gag gca tgc aga gag tta ggc ttt tct agc aac ttg 145
92 Glu Phe Ser Ser Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser Asn Leu
93 35 40 45
95 ctt tgc agc tct tgt gat ctt ctc gga cag ttc aac ctg ctt cag ctg 193
96 Leu Cys Ser Ser Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu Gln Leu
97 50 55 60
99 gat cct gat tgc aga gga tgc tgt cag gag gaa gca caa ttt gaa acc 241
100 Asp Pro Asp Cys Arg Gly Cys Cys Gln Glu Glu Ala Gln Phe Glu Thr
101 65 70 75
103 aaa aag ctg tat gca gga gct att ctt gaa gtt tgt gga tga aaa ttg 289
W--> 104 Lys Lys Leu Tyr Ala Gly Ala Ile Leu Glu Val Cys Gly Xaa Lys Leu
105 80 85 90 95
107 gga agg ttc cct caa gtc caa gct ttt gtt agg agt gat aaa ccc aaa 337
108 Gly Arg Phe Pro Gln Val Gln Ala Phe Val Arg Ser Asp Lys Pro Lys
109 100 105 110
111 ctg ttc aga gga ctg caa atc aag tat gtc cgt ggt tca gac cct gta 385
112 Leu Phe Arg Gly Leu Gln Ile Lys Tyr Val Arg Gly Ser Asp Pro Val
113 115 120 125
115 tta aag ctt ttg gac gac aat ggg aac att gct gaa gaa ctg agc att 433
116 Leu Lys Leu Leu Asp Asp Asn Gly Asn Ile Ala Glu Glu Leu Ser Ile
117 130 135 140
119 ctc aaa tgg aac aca gac agt gta gaa gaa ttc ctg agt gaa aag ttg 481
120 Leu Lys Trp Asn Thr Asp Ser Val Glu Glu Phe Leu Ser Glu Lys Leu
121 145 150 155
123 gaa cgc ata taa atottgctta aattttgtcc tatccttttg ttaccttacc 533
124 Glu Arg Ile
125 160
127 aaatgaaata ttacagcacc tagaaaataa tttagttttg cttgcttcca ttgatcagtc 593
129 ttttacttga ggcattaaat atctaattaa atcgtgaaat ggcagtatag tccatgatat 653
131 ctaaggagtt ggcaagctta acaaaaccca ttttttataa atgtccatcc tcctgcattt 713
133 gttgatacca ctaacaaat gctttgtaac agacttgagg ttaattatgc aaatgatagt 773
135 ttgtgataat tgggtccagt ttacgaacaa cagatttcta aattagagag gttacaaga 833
137 cagatgatta ctatgcctca tgtgctgtgt gctctttgaa aggaatgaca gcagactaca 893
139 aagcaataa gatatactga gcctcaacag attgcctgct cctcagagtc tctcctattt 953
141 ttgtattacc cagctttctt ttaatacaa atgttattta tagtttaca tgaatgcact 1013
143 gcataaaaac ttgtagctt cattattgta aaacatattc aagatcctac agtaagagtg 1073

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145 aaacattcac aaagatttgc gttaatgaag actacacaga aaacctttct agggatttgt 1133
147 gtggatcaga tacatacttg gcaaattttt gagttttaca ttcttacaga aaagtccatt 1193
149 taaaagtgat catttgtaag accaaaatat aaataaaaag tttcaaaaat c 1244
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153 <211> LENGTH: 489
154 <212> TYPE: DNA
155 <213> ORGANISM: Homo sapiens
157 <220> FEATURE:
158 <221> NAME/KEY: CDS
159 <222> LOCATION: (1)..(489)
161 <220> FEATURE:
162 <221> NAME/KEY: misc_feature
163 <222> LOCATION: (277)..(279)
164 <223> OTHER INFORMATION: TGA codon codes for Selenocysteine, Xaa
166 <400> SEQUENCE: 3
167 atg gcg gct ggg ccg agt ggg tgt ctg gtg ccg gcg ttt ggg cta cgg 48
168 Met Ala Ala Gly Pro Ser Gly Cys Leu Val Pro Ala Phe Gly Leu Arg
169 1 5 10 15
171 ttg ttg ttg gcg act gtg ctt caa gcg gtg tct gct ttt ggg gca gag 96
172 Leu Leu Leu Ala Thr Val Leu Gln Ala Val Ser Ala Phe Gly Ala Glu
173 20 25 30
175 ttt tca tcg gag gca tgc aga gag tta ggc ttt tct agc aac ttg ctt 144
176 Phe Ser Ser Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser Asn Leu Leu
177 35 40 45
179 tgc agc tct tgt gat ctt ctc gga cag ttc aac ctg ctt cag ctg gat 192
180 Cys Ser Ser Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu Gln Leu Asp
181 50 55 60
183 cct gat tgc aga gga tgc tgt cag gag gaa gca caa ttt gaa acc aaa 240
184 Pro Asp Cys Arg Gly Cys Cys Gln Glu Glu Ala Gln Phe Glu Thr Lys
185 65 70 75 80
187 aag ctg tat gca gga gct att ctt gaa gtt tgt gga tga aaa ttg gga 288
W--> 188 Lys Leu Tyr Ala Gly Ala Ile Leu Glu Val Cys Gly Xaa Lys Leu Gly
189 85 90 95
191 agg ttc cct caa gtc caa gct ttt gtt agg agt gat aaa ccc aaa ctg 336
192 Arg Phe Pro Gln Val Gln Ala Phe Val Arg Ser Asp Lys Pro Lys Leu
193 100 105 110
195 ttc aga gga ctg caa atc aag tat gtc cgt ggt tca gac cct gta tta 384
196 Phe Arg Gly Leu Gln Ile Lys Tyr Val Arg Gly Ser Asp Pro Val Leu
197 115 120 125
199 aag ctt ttg gac gac aat ggg aac att gct gaa gaa ctg agc att ctc 432
200 Lys Leu Leu Asp Asp Asn Gly Asn Ile Ala Glu Glu Leu Ser Ile Leu
201 130 135 140
203 aaa tgg aac aca gac agt gta gaa gaa ttc ctg agt gaa aag ttg gaa 480
204 Lys Trp Asn Thr Asp Ser Val Glu Glu Phe Leu Ser Glu Lys Leu Glu
205 145 150 155 160
207 cgc ata taa 489
208 Arg Ile
211 <210> SEQ ID NO: 4
212 <211> LENGTH: 136

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213 <212> TYPE: PRT
 214 <213> ORGANISM: Homo sapiens
 216 <220> FEATURE:
 217 <221> NAME/KEY: SITE
 218 <222> LOCATION: (67)
 219 <223> OTHER INFORMATION: Xaa is selenocysteine
 221 <400> SEQUENCE: 4
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 223 1 5 10 15
 225 Phe Ser Ser Asn Leu Leu Cys Ser Ser Cys Asp Leu Leu Gly Gln Phe
 226 20 25 30
 228 Asn Leu Leu Gln Leu Asp Pro Asp Cys Arg Gly Cys Cys Gln Glu Glu
 229 35 40 45
 231 Ala Gln Phe Glu Thr Lys Lys Leu Tyr Ala Gly Ala Ile Leu Glu Val
 232 50 55 60
 234 Cys Gly Xaa Lys Leu Gly Arg Phe Pro Gln Val Gln Ala Phe Val Arg
 235 65 70 75 80
 237 Ser Asp Lys Pro Lys Leu Phe Arg Gly Leu Gln Ile Lys Tyr Val Arg
 238 85 90 95
 240 Gly Ser Asp Pro Val Leu Lys Leu Leu Asp Asp Asn Gly Asn Ile Ala
 241 100 105 110
 243 Glu Glu Leu Ser Ile Leu Lys Trp Asn Thr Asp Ser Val Glu Glu Phe
 244 115 120 125
 246 Leu Ser Glu Lys Leu Glu Arg Ile
 247 130 135
 250 <210> SEQ ID NO: 5
 251 <211> LENGTH: 21
 252 <212> TYPE: DNA
 253 <213> ORGANISM: Artificial Sequence
 255 <220> FEATURE:
 256 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
 258 <400> SEQUENCE: 5
 259 atggcggctg ggccgagtgg g 21
 262 <210> SEQ ID NO: 6
 263 <211> LENGTH: 21
 264 <212> TYPE: DNA
 265 <213> ORGANISM: Artificial Sequence
 267 <220> FEATURE:
 268 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
 270 <400> SEQUENCE: 6
 271 taatatgcgt tccaactttt c 21
 274 <210> SEQ ID NO: 7
 275 <211> LENGTH: 21
 276 <212> TYPE: DNA
 277 <213> ORGANISM: Artificial Sequence
 279 <220> FEATURE:
 280 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
 282 <400> SEQUENCE: 7
 283 tctgcttttg ggcagagatt t 21

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Input Set : A:\56113.app
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286 <210> SEQ ID NO: 8
 287 <211> LENGTH: 1216
 288 <212> TYPE: DNA
 289 <213> ORGANISM: Mus musculus
 291 <220> FEATURE:
 292 <221> NAME/KEY: CDS
 293 <222> LOCATION: (11)..(490)
 295 <220> FEATURE:
 296 <221> NAME/KEY: misc_feature
 297 <222> LOCATION: (287)..(289)
 298 <223> OTHER INFORMATION: TGA codon codes for Selenocysteine, Xaa
 300 <400> SEQUENCE: 8
 301 gaccgcaggg atg gcg gca ggg cag ggt ggg tgg ctg cgg cca gct ctg 49
 302 Met Ala Ala Gly Gln Gly Gly Trp Leu Arg Pro Ala Leu
 303 1 5 10
 305 ggg ctg cgc ttg ctg ctg gcg act gcg ttt caa gcg gtg tct gct ctg 97
 306 Gly Leu Arg Leu Leu Leu Ala Thr Ala Phe Gln Ala Val Ser Ala Leu
 307 15 20 25
 309 ggg gca gag ttt gcg tca gag gca tgc aga gag ttg ggt ttc tcc agc 145
 310 Gly Ala Glu Phe Ala Ser Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser
 311 30 35 40 45
 313 aac ttg ctc tgc agc tct tgc gat ctt ctt gga cag ttt aat ctg ctc 193
 314 Asn Leu Leu Cys Ser Ser Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu
 315 50 55 60
 317 cca ctg gac cct gtt tgc aga ggg tgc tgt cag gaa gaa gca caa ttt 241
 318 Pro Leu Asp Pro Val Cys Arg Gly Cys Cys Gln Glu Glu Ala Gln Phe
 319 65 70 75
 321 gaa acc aaa aag ctg tat gca gga gcc atc ctt gaa gtc tgc gga tga 289
 322 Glu Thr Lys Lys Leu Tyr Ala Gly Ala Ile Leu Glu Val Cys Gly Xaa
 323 80 85 90
 325 aaa ttg ggg agg ttc cct caa gtc caa gct ttt gtc aga agt gat aaa 337
 326 Lys Leu Gly Arg Phe Pro Gln Val Gln Ala Phe Val Arg Ser Asp Lys
 327 95 100 105
 329 ccc aaa ctc ttc aga ggt cta cag atc aag tat gtt cga ggc tca gac 385
 330 Pro Lys Leu Phe Arg Gly Leu Gln Ile Lys Tyr Val Arg Gly Ser Asp
 331 110 115 120 125
 333 cct gta cta aag ctt ttg gac gac aac ggg aac att gct gaa gaa cta 433
 334 Pro Val Leu Lys Leu Leu Asp Asp Asn Gly Asn Ile Ala Glu Glu Leu
 335 130 135 140
 337 agc atc ctc aaa tgg aac aca gac agt gtg gaa gag ttc ctg agc gag 481
 338 Ser Ile Leu Lys Trp Asn Thr Asp Ser Val Glu Glu Phe Leu Ser Glu
 339 145 150 155
 341 aag ttg gaa cgcataataa catgcttagt agtttttata ctaatcaaat 530
 342 Lys Leu Glu
 343 160
 345 gaattatcac agcacctaga caataactta gttttgcatg cttacattgg tcatcctttt 590
 347 tatgtacatc attaatcttc tgacaagaag ctgaagtagc accacagtcc ataatatatc 650
 349 aggatctggc aagcttaagg aacccagctc ttagaaaattt ctcttcttct acacttggtg 710
 351 ctctcaccag tgaaacgctt tgtaaggagg catctgggta attatgcaa taagtttgtg 770

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Application Number
 L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:49 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
 L:104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
 L:188 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
 L:234 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
 L:322 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
 L:396 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9